

SEQUENCE LISTING IAP20 REGD TCT/TTT 13 DEC 2005

<110> Lassen, Soren Flensted
 <120> Improved proteases and methods for producing them
 <130> 10423.204-US
 <160> 53
 <170> PatentIn version 3.3
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 <211> 1062
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 <213> Nocardiosis sp. NRRL 18262
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 <222> (1)..(495)
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 <222> (496)..(1059)
 <223> Encodes the mature region shown in positions 1-188 of SEQ ID NO:43.
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<210> 2
 <211> 1143
 <212> DNA
 <213> Artificial sequence

<220>
 <223> A synthetic 10R gene (10Rsyntax-15) encoding a S2A protease denoted "10R" fused by PCR in frame to the signal peptide encoding sequence of a heterologous protease, Savinase.

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taa 1143

<210> 3

<211> 8

<212> PRT

<213> Artificial sequence

<220>

<223> C-terminal amino acid tail expressed as fusion to protease of the invention.

<400> 3

Gln Ser His Val Gln Ser Ala Pro

1

5

<210> 4

<211> 24

<212> DNA

<213> Artificial sequence

<220>

<223> Polynucleotide encoding a C-terminal amino acid tail expressed as fusion to protease of the invention.

<400> 4

caatcgcgatg ttcaatccgc tcca

24

<210> 5

<211> 4

<212> PRT

<213> Artificial sequence

<220>

<223> C-terminal amino acid tail expressed as fusion to protease of the invention.

<400> 5

Gln Ser Ala Pro

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<210> 6

<211> 12

<212> DNA

<213> Artificial sequence

<220>

<223> Polynucleotide encoding a C-terminal amino acid tail expressed as fusion to protease of the invention.

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12

<210> 7
<211> 2
<212> PRT
<213> Artificial sequence

<220>
<223> C-terminal amino acid tail expressed as fusion to protease of the invention.

<400> 7

Gln Pro
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<210> 8
<211> 6
<212> DNA
<213> Artificial sequence

<220>
<223> Polynucleotide encoding a C-terminal amino acid tail expressed as fusion to protease of the invention.

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<210> 9
<211> 1
<212> PRT
<213> Artificial sequence

<220>
<223> C-terminal amino acid tail expressed as fusion to protease of the invention.

<400> 9

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<210> 10
<211> 3
<212> DNA
<213> Artificial sequence

<220>
<223> Polynucleotide encoding a C-terminal amino acid tail expressed as fusion to protease of the invention.

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<210> 11
 <211> 45
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Primer #252639

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<210> 12
 <211> 44
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Primer #251992

<400> 12
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<210> 13
 <211> 44
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Primer #179541

<400> 13
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<210> 14
 <211> 43
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Primer #179542

<400> 14
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<210> 15
 <211> 64
 <212> DNA
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<220>
 <223> Primer #179539

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 atcc 64

 <210> 16
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 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Primer #179540

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 <223> Primer #179154

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 <210> 18
 <211> 37
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Primer #179153

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 <210> 19
 <211> 22
 <212> DNA
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 <220>
 <223> Primer #317

 <400> 19
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<210> 20
 <211> 40
 <212> DNA
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<220>
 <223> Primer #139 NotI

<400> 20
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<210> 21
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<220>
 <223> Sequence of plasmid pMB1508

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<220>
 <223> Sequence of MB1510 genomic integration region

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cggttccatt tttccctg 5718

<210> 23
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> Primer 1605

<400> 23
gacggccagt gaattcgata aaagtgc 27

<210> 24
<211> 42
<212> DNA
<213> Artificial sequence

<220>
<223> Primer 1606

<220>
<221> misc_feature
<222> (13)..(13)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (16)..(16)
<223> n is a, c, g, or t

<400> 24
ccagatctct atnktntgt acggagtcta actccccaag ag 42

<210> 25
<211> 1112
<212> DNA
<213> Nocardiosis dassonvillei DSM 43235

<400> 25
gcttttagtt catcgatcgc atcggctgct ccggcccccg tccccagac cccggtcgcc 60
gacgacagcg ccgccagcat gaccgaggcg ctcaagcgcg acctcgacct cacctcggcc 120
gaggccgagg agcttctctc ggcgaggaa gccgccatcg agaccgacgc cgaggccacc 180
gaggccgcg gcgaggccta cggcggtcga ctgttcgaca ccgagaccct cgaactcacc 240
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<211> 48
<212> DNA
<213> Artificial sequence

<220>
<223> Primer 1423

<400> 26
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<210> 27
<211> 45
<212> DNA
<213> Artificial sequence

<220>

<223> Primer 1475

<400> 27

ggagcggatt gaacatgcga ttaggtccgg atcctgacac cccag

45

<210> 28

<211> 354

<212> PRT

<213> Nocardiosis dassonvillei DSM 43235

<220>

<221> PROPEP

<222> (1)..(166)

<220>

<221> mat_peptide

<222> (167)..(354)

<400> 28

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-165 -160 -155

Ala Ser Met Thr Glu Ala Leu Lys Arg Asp Leu Asp Leu Thr Ser
-150 -145 -140

Ala Glu Ala Glu Glu Leu Leu Ser Ala Gln Glu Ala Ala Ile Glu
-135 -130 -125

Thr Asp Ala Glu Ala Thr Glu Ala Ala Gly Glu Ala Tyr Gly Gly
-120 -115 -110

Ser Leu Phe Asp Thr Glu Thr Leu Glu Leu Thr Val Leu Val Thr Asp
-105 -100 -95

Ala Ser Ala Val Glu Ala Val Glu Ala Thr Gly Ala Gln Ala Thr Val
-90 -85 -80 -75

Val Ser His Gly Thr Glu Gly Leu Thr Glu Val Val Glu Asp Leu Asn
-70 -65 -60

Gly Ala Glu Val Pro Glu Ser Val Leu Gly Trp Tyr Pro Asp Val Glu
-55 -50 -45

Ser Asp Thr Val Val Val Glu Val Leu Glu Gly Ser Asp Ala Asp Val

-40 -35 -30
 Ala Ala Leu Leu Ala Asp Ala Gly Val Asp Ser Ser Ser Val Arg Val
 -25 -20 -15
 Glu Glu Ala Glu Glu Ala Pro Gln Val Tyr Ala Asp Ile Ile Gly Gly
 -10 -5 -1 1 5
 Leu Ala Tyr Tyr Met Gly Gly Arg Cys Ser Val Gly Phe Ala Ala Thr
 10 15 20
 Asn Ser Ala Gly Gln Pro Gly Phe Val Thr Ala Gly His Cys Gly Thr
 25 30 35
 Val Gly Thr Gly Val Thr Ile Gly Asn Gly Thr Gly Thr Phe Gln Asn
 40 45 50
 Ser Val Phe Pro Gly Asn Asp Ala Ala Phe Val Arg Gly Thr Ser Asn
 55 60 65 70
 Phe Thr Leu Thr Asn Leu Val Ser Arg Tyr Asn Ser Gly Gly Tyr Gln
 75 80 85
 Ser Val Thr Gly Thr Ser Gln Ala Pro Ala Gly Ser Ala Val Cys Arg
 90 95 100
 Ser Gly Ser Thr Thr Gly Trp His Cys Gly Thr Ile Gln Ala Arg Asn
 105 110 115
 Gln Thr Val Arg Tyr Pro Gln Gly Thr Val Tyr Ser Leu Thr Arg Thr
 120 125 130
 Asn Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Phe Ile Ser Gly
 135 140 145 150
 Ser Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly Asn Cys Ser Val
 155 160 165
 Gly Gly Thr Thr Tyr Tyr Gln Glu Val Thr Pro Met Ile Asn Ser Trp
 170 175 180
 Gly Val Arg Ile Arg Thr
 185

<210> 29
 <211> 498
 <212> DNA
 <213> Nocardiosis dassonvillei DSM 43235

<400> 29
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 gaagccgcca tcgagaccga cgccgaggcc accgaggccg cgggcgaggc ctacggcggc 180
 tcaactgttcg acaccgagac cctcgaactc accgtgctgg tcaccgacgc ctccgccgtc 240
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 ccggacgtgg agagcgacac cgtcgtggtc gaggtgctgg agggctccga cgccgacgtc 420
 gccgccctgc tcgccgacgc cgggtgtggac tctcctcgg tccgggtgga ggaggccgag 480
 gaggccccgc aggtctac 498

<210> 30
 <211> 166
 <212> PRT
 <213> Nocardiosis dassonvillei DSM 43235

<400> 30

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Ser	Met	Thr	Glu	Ala	Leu	Lys	Arg	Asp	Leu	Asp	Leu	Thr	Ser	Ala	Glu
			20					25					30		
Ala	Glu	Glu	Leu	Leu	Ser	Ala	Gln	Glu	Ala	Ala	Ile	Glu	Thr	Asp	Ala
			35				40					45			
Glu	Ala	Thr	Glu	Ala	Ala	Gly	Glu	Ala	Tyr	Gly	Gly	Ser	Leu	Phe	Asp
	50					55					60				
Thr	Glu	Thr	Leu	Glu	Leu	Thr	Val	Leu	Val	Thr	Asp	Ala	Ser	Ala	Val
65					70					75				80	
Glu	Ala	Val	Glu	Ala	Thr	Gly	Ala	Gln	Ala	Thr	Val	Val	Ser	His	Gly
			85					90						95	

Thr Glu Gly Leu Thr Glu Val Val Glu Asp Leu Asn Gly Ala Glu Val
100 105 110

Pro Glu Ser Val Leu Gly Trp Tyr Pro Asp Val Glu Ser Asp Thr Val
115 120 125

Val Val Glu Val Leu Glu Gly Ser Asp Ala Asp Val Ala Ala Leu Leu
130 135 140

Ala Asp Ala Gly Val Asp Ser Ser Ser Val Arg Val Glu Glu Ala Glu
145 150 155 160

Glu Ala Pro Gln Val Tyr
165

<210> 31
<211> 1146
<212> DNA
<213> Artificial sequence

<220>
<223> The DNA sequence coding for the pro-region of SEQ ID NO: 29 fused
in frame to A1918L2 protease tail-variant encoding gene; whole
construct: 10R(proA1918L2).

<400> 31
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agcgccgcca gcatgaccga ggcgctcaag cgcgacctcg acctcacctc ggccgaggcc 180
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gtccgggttg aggaggccga ggaggccccg caggtctatg ccgatatcat tggaggccta 600
gcgtacacaa tgggtggtcg ctgcagcgta ggatttgag ccacaaatgc agctggacaa 660
cctggcttcg tgacagctgg acattgcggc cgcgtcggta cacaggttac tatcggcaat 720
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acgtccaact ttacgcttac taacttagta tctagatata acactggcgg atatgcaact	840
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ggatggcatt gtggaaccat tcaagctaga ggtcagagcg tgagctatcc tgaaggtacc	960
gtaacgaaca tgactcgtac gactgtatgt gcagaaccag gtgactctgg aggttcatat	1020
atcagcggta cgcaagcgca aggcgttacc tcaggtggat ccggttaactg taggacaggt	1080
ggcacaacgt tctaccagga agtgacaccg atggtgaact cttggggagt tagactccgt	1140
acataa	1146

<210> 32

<211> 1068

<212> DNA

<213> Nocardiosis Alba DSM 15647

<400> 32

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gaggccctcc agcgcgacct cggcctgtcc ccctctcagg ccgacgagct cctcgaggcg	120
caggccgagt ccttcgagat cgacgaggcc gccaccgcgg ccgcagccga ctctacggc	180
ggctccatct tcgacaccga cagcctcacc ctgaccgtcc tggtcaccga cgcctccgcc	240
gtcgaggcgg tcgaggccgc cggcgccgag gccaaagggtg tctcgcacgg catggagggc	300
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taccccgaca tccactccga cacggtcgtc ctcgaggctc tcgagggtc cggtgccgac	420
gtggactccc tgctcgccga cgccggtgtg gacaccgccg acgtcaaggt ggagagcacc	480
accgagcagc ccgagctgta cgccgacatc atcggcggtc tcgcctacac catgggtggg	540
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accaacctgg tcagccgcta caacaccggt ggttacgcga ccgtctccgg ctctcgag	780
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cagggcgta cctccgggtg ctccggcaac tgctccttcg gtggcaccac ctactaccag	1020
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<210> 33
 <211> 355
 <212> PRT
 <213> Nocardiosis Alba DSM 15647

<220>
 <221> PROPEP
 <222> (1)..(167)

<220>
 <221> mat_peptide
 <222> (168)..(355)

<400> 33

Ala Thr Gly Pro Leu Pro Gln Ser Pro Thr Pro Asp Glu Ala Glu
 -165 -160 -155

Ala Thr Thr Met Val Glu Ala Leu Gln Arg Asp Leu Gly Leu Ser
 -150 -145 -140

Pro Ser Gln Ala Asp Glu Leu Leu Glu Ala Gln Ala Glu Ser Phe
 -135 -130 -125

Glu Ile Asp Glu Ala Ala Thr Ala Ala Ala Ala Asp Ser Tyr Gly
 -120 -115 -110

Gly Ser Ile Phe Asp Thr Asp Ser Leu Thr Leu Thr Val Leu Val Thr
 -105 -100 -95

Asp Ala Ser Ala Val Glu Ala Val Glu Ala Ala Gly Ala Glu Ala Lys
 -90 -85 -80

Val Val Ser His Gly Met Glu Gly Leu Glu Glu Ile Val Ala Asp Leu
 -75 -70 -65 -60

Asn Ala Ala Asp Ala Gln Pro Gly Val Val Gly Trp Tyr Pro Asp Ile
 -55 -50 -45

His Ser Asp Thr Val Val Leu Glu Val Leu Glu Gly Ser Gly Ala Asp
 -40 -35 -30

Val Asp Ser Leu Leu Ala Asp Ala Gly Val Asp Thr Ala Asp Val Lys
 -25 -20 -15

Val Glu Ser Thr Thr Glu Gln Pro Glu Leu Tyr Ala Asp Ile Ile Gly
 -10 -5 -1 1 5

Gly Leu Ala Tyr Thr Met Gly Gly Arg Cys Ser Val Gly Phe Ala Ala
 10 15 20

Thr Asn Ala Ser Gly Gln Pro Gly Phe Val Thr Ala Gly His Cys Gly
 25 30 35

Thr Val Gly Thr Pro Val Ser Ile Gly Asn Gly Gln Gly Val Phe Glu
 40 45 50

Arg Ser Val Phe Pro Gly Asn Asp Ser Ala Phe Val Arg Gly Thr Ser
 55 60 65

Asn Phe Thr Leu Thr Asn Leu Val Ser Arg Tyr Asn Thr Gly Gly Tyr
 70 75 80 85

Ala Thr Val Ser Gly Ser Ser Gln Ala Ala Ile Gly Ser Gln Ile Cys
 90 95 100

Arg Ser Gly Ser Thr Thr Gly Trp His Cys Gly Thr Val Gln Ala Arg
 105 110 115

Gly Gln Thr Val Ser Tyr Pro Gln Gly Thr Val Gln Asn Leu Thr Arg
 120 125 130

Thr Asn Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Phe Ile Ser
 135 140 145

Gly Ser Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly Asn Cys Ser
 150 155 160 165

Phe Gly Gly Thr Thr Tyr Tyr Gln Glu Val Asn Pro Met Leu Ser Ser
 170 175 180

Trp Gly Leu Thr Leu Arg Thr
 185

<210> 34
 <211> 43
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Primer 1421

<400> 34
 gttcatcgat cgcacggtg ggcacggcc cctccccca gtc 43

<210> 35
 <211> 31
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Primer 1604

<400> 35
 gcggtaccta tcaggtgagc agggtcagac c 31

<210> 36
 <211> 1062
 <212> DNA
 <213> Nocardiosis prasina DSM 15648

<400> 36
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 gcgctccagc gcgacctcg cctgaccccg cttgaggccg atgaactgct ggccgcccag 120
 gacaccgcct tcgaggtcga cgaggccgag gccgcggccg ccgggggacgc ctacggcggc 180
 tccgtcttcg acaccgagac cctggaactg accgtccttg tcaccgacgc cgcctcggtc 240
 gaggtctgtg aggccaccg cgcggtgacc gaactcgtct cctacggcat cgagggcctc 300
 gacgagatca tccaggatct caacgccgac gacgccgtcc ccggcgtggt cggctggtac 360
 ccggacgtgg cgggtgacac cgtcgtcctg gaggtccttg agggttccg agccgacgtg 420
 agcggcctgc tcgccgacgc cggcgtggac gcctcggccg tcgaggtgac cagcagtgcg 480
 cagcccagac tctacgccga catcatcggc ggtctggcct acaccatggg cggccgctgt 540
 tcggtcggat tcgcggccac caacgccgac ggtcagccc gattcgtcac cgccggtcac 600
 tgtggccgag tgggcaccca ggtgagcatc ggcaacggcc agggcgtctt cgagcagtcc 660
 atcttcccgg gcaacgacgc cgccttcgtc cgcggcacgt ccaacttcac gctgaccaac 720
 ctggtcagcc gctacaacac cggcggttac gccaccgtcg ccggccacaa ccaggcgccc 780
 atcggctcct ccgtctgccc ctccgggtcc accaccggct ggcactgcgg caccatccag 840
 gcccgcgcc agtcggtgag ctaccccgag ggcaccgtca ccaacatgac ccggaccacc 900
 gtgtgcgccc agcccggcga ctccggcggc tcctacatct ccggcaacca ggcccagggc 960

gtcacctccg gcgggtccgg caactgccgc accggcggga ccaccttcta ccaggaggtc 1020

accccatgg tgaactcctg gggcgtccgt ctccggacct aa 1062

<210> 37

<211> 353

<212> PRT

<213> Nocardiosis prasina DSM 15648

<220>

<221> PROPEP

<222> (1)..(165)

<220>

<221> mat_peptide

<222> (166)..(353)

<400> 37

Ala Thr Gly Pro Leu Pro Gln Ser Pro Thr Pro Glu Ala Asp Ala
-165 -160 -155

Val Ser Met Gln Glu Ala Leu Gln Arg Asp Leu Gly Leu Thr Pro
-150 -145 -140

Leu Glu Ala Asp Glu Leu Leu Ala Ala Gln Asp Thr Ala Phe Glu
-135 -130 -125

Val Asp Glu Ala Ala Ala Ala Ala Ala Gly Asp Ala Tyr Gly Gly
-120 -115 -110

Ser Val Phe Asp Thr Glu Thr Leu Glu Leu Thr Val Leu Val Thr Asp
-105 -100 -95 -90

Ala Ala Ser Val Glu Ala Val Glu Ala Thr Gly Ala Gly Thr Glu Leu
-85 -80 -75

Val Ser Tyr Gly Ile Glu Gly Leu Asp Glu Ile Ile Gln Asp Leu Asn
-70 -65 -60

Ala Ala Asp Ala Val Pro Gly Val Val Gly Trp Tyr Pro Asp Val Ala
-55 -50 -45

Gly Asp Thr Val Val Leu Glu Val Leu Glu Gly Ser Gly Ala Asp Val
-40 -35 -30

Ser Gly Leu Leu Ala Asp Ala Gly Val Asp Ala Ser Ala Val Glu Val
 -25 -20 -15 -10

Thr Ser Ser Ala Gln Pro Glu Leu Tyr Ala Asp Ile Ile Gly Gly Leu
 -5 -1 1 5

Ala Tyr Thr Met Gly Gly Arg Cys Ser Val Gly Phe Ala Ala Thr Asn
 10 15 20

Ala Ala Gly Gln Pro Gly Phe Val Thr Ala Gly His Cys Gly Arg Val
 25 30 35

Gly Thr Gln Val Ser Ile Gly Asn Gly Gln Gly Val Phe Glu Gln Ser
 40 45 50 55

Ile Phe Pro Gly Asn Asp Ala Ala Phe Val Arg Gly Thr Ser Asn Phe
 60 65 70

Thr Leu Thr Asn Leu Val Ser Arg Tyr Asn Thr Gly Gly Tyr Ala Thr
 75 80 85

Val Ala Gly His Asn Gln Ala Pro Ile Gly Ser Ser Val Cys Arg Ser
 90 95 100

Gly Ser Thr Thr Gly Trp His Cys Gly Thr Ile Gln Ala Arg Gly Gln
 105 110 115

Ser Val Ser Tyr Pro Glu Gly Thr Val Thr Asn Met Thr Arg Thr Thr
 120 125 130 135

Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Tyr Ile Ser Gly Asn
 140 145 150

Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr Gly
 155 160 165

Gly Thr Thr Phe Tyr Gln Glu Val Thr Pro Met Val Asn Ser Trp Gly
 170 175 180

Val Arg Leu Arg Thr
 185

<210> 38
 <211> 43
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Primer 1346

 <400> 38
 gttcatcgat cgcacggct gccaccggac cgctcccca gtc 43

 <210> 39
 <211> 38
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Primer 1602

 <400> 39
 gcggatccta ttaggtccgg agacggacgc cccaggag 38

 <210> 40
 <211> 1062
 <212> DNA
 <213> Nocardiosis prasina DSM 15649

 <400> 40
 gccaccggac cactcccca gtcaccacc ccggaggccg acgccgtctc catgcaggag 60
 gcgctccagc gcgacctcg cctgaccccg cttgaggccg atgaactgct ggccgcccag 120
 gacaccgcct tcgaggtcga cgaggcccg gccgaggccg ccggtgacgc ctacggcggc 180
 tccgtcttcg acaccgagac cctggaactg accgtccttg tcaccgactc cgccgcggtc 240
 gaggcggtgg aggccaccgg cgccgggacc gaactggtct cctacggcat cacgggcctc 300
 gacgagatcg tcgaggagct caacgccgcc gacgccgttc ccggcggtgg cggctggtac 360
 ccggacgtcg cgggtgacac cgtcgtgctg gaggtccttg agggttccgg cgccgacgtg 420
 ggccggcctgc tcgccgacgc cggcgtggac gcctcggcgg tcgaggtgac caccaccgag 480
 cagcccagac tgtacgccga catcatcggc ggtctggcct acaccatggg cgccgctgt 540
 tcggtcggct tcgcggccac caacgccgcc ggtcagcccg ggttcgtcac cgccggtcac 600
 tgtggcccg tgggcaccca ggtgaccatc ggcaacggcc gggcgctctt cgagcagtcc 660
 atcttcccgg gcaacgacgc cgccttcgtc cgcggaacgt ccaacttcac gctgaccaac 720
 ctggtcagcc gctacaacac cggcggttac gccaccgtcg ccggtcacia ccaggcgccc 780
 atcggctcct ccgtctgccg ctccgggtcc accaccggtt ggcaactgcg caccatccag 840

gcccgcggcc agtcggtgag ctaccccgag ggcaccgtca ccaacatgac gcggaccacc 900
gtgtgcgccg agcccggcga ctccggcggc tctacatct cgggcaacca ggcccagggc 960
gtcacctccg gcggctccgg caactgccgc accggcggga ccaccttcta ccaggaggtc 1020
accccatgg tgaactcctg gggcgctcgt ctccggacct aa 1062

<210> 41
<211> 353
<212> PRT
<213> Nocardiosis prasina DSM 15649

<220>
<221> PROPEP
<222> (1)..(165)

<220>
<221> mat_peptide
<222> (166)..(353)

<400> 41

Ala Thr Gly Pro Leu Pro Gln Ser Pro Thr Pro Glu Ala Asp Ala
-165 -160 -155

Val Ser Met Gln Glu Ala Leu Gln Arg Asp Leu Gly Leu Thr Pro
-150 -145 -140

Leu Glu Ala Asp Glu Leu Leu Ala Ala Gln Asp Thr Ala Phe Glu
-135 -130 -125

Val Asp Glu Ala Ala Ala Glu Ala Ala Gly Asp Ala Tyr Gly Gly
-120 -115 -110

Ser Val Phe Asp Thr Glu Thr Leu Glu Leu Thr Val Leu Val Thr Asp
-105 -100 -95 -90

Ser Ala Ala Val Glu Ala Val Glu Ala Thr Gly Ala Gly Thr Glu Leu
-85 -80 -75

Val Ser Tyr Gly Ile Thr Gly Leu Asp Glu Ile Val Glu Glu Leu Asn
-70 -65 -60

Ala Ala Asp Ala Val Pro Gly Val Val Gly Trp Tyr Pro Asp Val Ala
-55 -50 -45

Gly Asp Thr Val Val Leu Glu Val Leu Glu Gly Ser Gly Ala Asp Val
 -40 -35 -30

Gly Gly Leu Leu Ala Asp Ala Gly Val Asp Ala Ser Ala Val Glu Val
 -25 -20 -15 -10

Thr Thr Thr Glu Gln Pro Glu Leu Tyr Ala Asp Ile Ile Gly Gly Leu
 -5 -1 1 5

Ala Tyr Thr Met Gly Gly Arg Cys Ser Val Gly Phe Ala Ala Thr Asn
 10 15 20

Ala Ala Gly Gln Pro Gly Phe Val Thr Ala Gly His Cys Gly Arg Val
 25 30 35

Gly Thr Gln Val Thr Ile Gly Asn Gly Arg Gly Val Phe Glu Gln Ser
 40 45 50 55

Ile Phe Pro Gly Asn Asp Ala Ala Phe Val Arg Gly Thr Ser Asn Phe
 60 65 70

Thr Leu Thr Asn Leu Val Ser Arg Tyr Asn Thr Gly Gly Tyr Ala Thr
 75 80 85

Val Ala Gly His Asn Gln Ala Pro Ile Gly Ser Ser Val Cys Arg Ser
 90 95 100

Gly Ser Thr Thr Gly Trp His Cys Gly Thr Ile Gln Ala Arg Gly Gln
 105 110 115

Ser Val Ser Tyr Pro Glu Gly Thr Val Thr Asn Met Thr Arg Thr Thr
 120 125 130 135

Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Tyr Ile Ser Gly Asn
 140 145 150

Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr Gly
 155 160 165

Gly Thr Thr Phe Tyr Gln Glu Val Thr Pro Met Val Asn Ser Trp Gly
 170 175 180

Val Arg Leu Arg Thr
185

<210> 42
<211> 43
<212> DNA
<213> Artificial sequence

<220>
<223> Primer 1603

<400> 42
gttcatcgat cgcacgcggct gccaccggac cactccccca gtc

43

<210> 43
<211> 353
<212> PRT
<213> Nocardiosis sp. NRRL 18262

<220>
<221> PROPEP
<222> (1)..(165)

<220>
<221> mat_peptide
<222> (166)..(1059)

<400> 43

Ala Thr Gly Ala Leu Pro Gln Ser Pro Thr Pro Glu Ala Asp Ala
-165 -160 -155

Val Ser Met Gln Glu Ala Leu Gln Arg Asp Leu Asp Leu Thr Ser
-150 -145 -140

Ala Glu Ala Glu Glu Leu Leu Ala Ala Gln Asp Thr Ala Phe Glu
-135 -130 -125

Val Asp Glu Ala Ala Ala Glu Ala Ala Gly Asp Ala Tyr Gly Gly
-120 -115 -110

Ser Val Phe Asp Thr Glu Ser Leu Glu Leu Thr Val Leu Val Thr Asp
-105 -100 -95 -90

Ala Ala Ala Val Glu Ala Val Glu Ala Thr Gly Ala Gly Thr Glu Leu
-85 -80 -75

Val Ser Tyr Gly Ile Asp Gly Leu Asp Glu Ile Val Gln Glu Leu Asn

-70	-65	-60
Ala Ala Asp Ala Val Pro Gly Val Val Gly Trp Tyr Pro Asp Val Ala		
-55	-50	-45
Gly Asp Thr Val Val Leu Glu Val Leu Glu Gly Ser Gly Ala Asp Val		
-40	-35	-30
Ser Gly Leu Leu Ala Asp Ala Gly Val Asp Ala Ser Ala Val Glu Val		
-25	-20	-15
Thr Thr Ser Asp Gln Pro Glu Leu Tyr Ala Asp Ile Ile Gly Gly Leu		
-5	-1 1	5
Ala Tyr Thr Met Gly Gly Arg Cys Ser Val Gly Phe Ala Ala Thr Asn		
10	15	20
Ala Ala Gly Gln Pro Gly Phe Val Thr Ala Gly His Cys Gly Arg Val		
25	30	35
Gly Thr Gln Val Thr Ile Gly Asn Gly Arg Gly Val Phe Glu Gln Ser		
40	45	50
Val Phe Pro Gly Asn Asp Ala Ala Phe Val Arg Gly Thr Ser Asn Phe		
60	65	70
Thr Leu Thr Asn Leu Val Ser Arg Tyr Asn Thr Gly Gly Tyr Ala Thr		
75	80	85
Val Ala Gly His Asn Gln Ala Pro Ile Gly Ser Ser Val Cys Arg Ser		
90	95	100
Gly Ser Thr Thr Gly Trp His Cys Gly Thr Ile Gln Ala Arg Gly Gln		
105	110	115
Ser Val Ser Tyr Pro Glu Gly Thr Val Thr Asn Met Thr Arg Thr Thr		
120	125	130
Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Tyr Ile Ser Gly Thr		
140	145	150
Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr Gly		
155	160	165

Gly Thr Thr Phe Tyr Gln Glu Val Thr Pro Met Val Asn Ser Trp Gly
170 175 180

Val Arg Leu Arg Thr
185

<210> 44
<211> 1164
<212> DNA
<213> artificial sequence

<220>
<223> Synthetic protease encoding gene

<220>
<221> CDS
<222> (1)..(1164)
<223> Full length protease

<220>
<221> sig_peptide
<222> (1)..(81)

<220>
<221> misc_feature
<222> (82)..(1164)
<223> Propeptide

<220>
<221> mat_peptide
<222> (577)..(1164)

<400> 44		
atg aaa aaa ccg ctg gga aaa att gtc gca agc aca gca ctt ctt		45
Met Lys Lys Pro Leu Gly Lys Ile Val Ala Ser Thr Ala Leu Leu		
-190 -185 -180		
att tca gtg gca ttt agc tca tct att gca tca gca gct aca gga		90
Ile Ser Val Ala Phe Ser Ser Ser Ile Ala Ser Ala Ala Thr Gly		
-175 -170 -165		
gca tta ccg cag tct ccg aca ccg gaa gca gat gca gtc tca atg		135
Ala Leu Pro Gln Ser Pro Thr Pro Glu Ala Asp Ala Val Ser Met		
-160 -155 -150		
caa gaa gca ctg caa aga gat ctt gat ctt aca tca gca gaa gca		180
Gln Glu Ala Leu Gln Arg Asp Leu Asp Leu Thr Ser Ala Glu Ala		
-145 -140 -135		
gaa gaa ctt ctt gct gca caa gat aca gca ttt gaa gtg gat gaa		225
Glu Glu Leu Leu Ala Ala Gln Asp Thr Ala Phe Glu Val Asp Glu		
-130 -125 -120		

gca gcg gca gaa gca gca gga gat gca tat ggc ggc tca gtt ttt Ala Ala Ala Glu Ala Ala Gly Asp Ala Tyr Gly Gly Ser Val Phe -115 -110 -105	270
gat aca gaa tca ctt gaa ctt aca gtt ctt gtt aca gat gca gca gca Asp Thr Glu Ser Leu Glu Leu Thr Val Leu Val Thr Asp Ala Ala Ala -100 -95 -90	318
gtt gaa gca gtt gaa gca aca gga gca gga aca gta ctt gtt tca tat Val Glu Ala Val Glu Ala Thr Gly Ala Gly Thr Val Leu Val Ser Tyr -85 -80 -75	366
gga att gat ggc ctt gat gaa att gtt caa gaa ctg aat gca gct gat Gly Ile Asp Gly Leu Asp Glu Ile Val Gln Glu Leu Asn Ala Ala Asp -70 -65 -60 -55	414
gct gtt ccg ggc gtt gtt ggc tgg tat ccg gat gtt gct gga gat aca Ala Val Pro Gly Val Val Gly Trp Tyr Pro Asp Val Ala Gly Asp Thr -50 -45 -40	462
gtt gtc ctt gaa gtt ctt gaa gga tca ggc gca gat gtt tca ggc ctg Val Val Leu Glu Val Leu Glu Gly Ser Gly Ala Asp Val Ser Gly Leu -35 -30 -25	510
ctg gca gac gca gga gtc gat gca tca gca gtt gaa gtt aca aca tca Leu Ala Asp Ala Gly Val Asp Ala Ser Ala Val Glu Val Thr Thr Ser -20 -15 -10	558
gat caa ccg gaa ctt tat gca gat att att ggc ggc ctg gca tat tat Asp Gln Pro Glu Leu Tyr Ala Asp Ile Ile Gly Gly Leu Ala Tyr Tyr -5 -1 1 5 10	606
atg ggc ggc aga tgc agc gtt ggc ttt gca gca aca aat gca tca ggc Met Gly Gly Arg Cys Ser Val Gly Phe Ala Ala Thr Asn Ala Ser Gly 15 20 25	654
caa ccg ggc ttt gtt aca gca ggc cat tgc ggc aca gtt ggc aca cca Gln Pro Gly Phe Val Thr Ala Gly His Cys Gly Thr Val Gly Thr Pro 30 35 40	702
gtt tca att ggc aat ggc aaa ggc gtt ttt gaa cga agc att ttt ccg Val Ser Ile Gly Asn Gly Lys Gly Val Phe Glu Arg Ser Ile Phe Pro 45 50 55	750
ggc aat gat tca gca ttt gtt aga ggc aca tca aat ttt aca ctt aca Gly Asn Asp Ser Ala Phe Val Arg Gly Thr Ser Asn Phe Thr Leu Thr 60 65 70	798
aat ctg gtt tca aga tat aat tca ggc ggc tat gca aca gtt gca ggc Asn Leu Val Ser Arg Tyr Asn Ser Gly Gly Tyr Ala Thr Val Ala Gly 75 80 85 90	846
cat aat caa gca ccg att ggc tca gca gtt tgc aga tca ggc tca aca His Asn Gln Ala Pro Ile Gly Ser Ala Val Cys Arg Ser Gly Ser Thr 95 100 105	894

aca ggc tgg cat tgc ggc aca att caa gca aga aat caa aca gtt agg 942
 Thr Gly Trp His Cys Gly Thr Ile Gln Ala Arg Asn Gln Thr Val Arg
 110 115 120

tat ccg caa ggc aca gtt tat agt ctg aca aga aca aca gtt tgt gca 990
 Tyr Pro Gln Gly Thr Val Tyr Ser Leu Thr Arg Thr Thr Val Cys Ala
 125 130 135

gaa ccg ggc gat tca ggc ggc tca tat att agc ggc act caa gca caa 1038
 Glu Pro Gly Asp Ser Gly Gly Ser Tyr Ile Ser Gly Thr Gln Ala Gln
 140 145 150

ggc gtt aca tca ggc ggc tca ggc aat tgc agt gct ggc ggc aca aca 1086
 Gly Val Thr Ser Gly Gly Ser Gly Asn Cys Ser Ala Gly Gly Thr Thr
 155 160 165 170

tat tac caa gaa gtt aat ccg atg ctt agt tca tgg ggc ctt aca ctt 1134
 Tyr Tyr Gln Glu Val Asn Pro Met Leu Ser Ser Trp Gly Leu Thr Leu
 175 180 185

aga aca caa tcg cat gtt caa tcc gct cca 1164
 Arg Thr Gln Ser His Val Gln Ser Ala Pro
 190 195

<210> 45
 <211> 388
 <212> PRT
 <213> artificial sequence

<220>
 <223> Synthetic Construct

<400> 45

Met Lys Lys Pro Leu Gly Lys Ile Val Ala Ser Thr Ala Leu Leu
 -190 -185 -180

Ile Ser Val Ala Phe Ser Ser Ser Ile Ala Ser Ala Ala Thr Gly
 -175 -170 -165

Ala Leu Pro Gln Ser Pro Thr Pro Glu Ala Asp Ala Val Ser Met
 -160 -155 -150

Gln Glu Ala Leu Gln Arg Asp Leu Asp Leu Thr Ser Ala Glu Ala
 -145 -140 -135

Glu Glu Leu Leu Ala Ala Gln Asp Thr Ala Phe Glu Val Asp Glu
 -130 -125 -120

Ala Ala Ala Glu Ala Ala Gly Asp Ala Tyr Gly Gly Ser Val Phe
 -115 -110 -105

Asp Thr Glu Ser Leu Glu Leu Thr Val Leu Val Thr Asp Ala Ala Ala
 -100 -95 -90

Val Glu Ala Val Glu Ala Thr Gly Ala Gly Thr Val Leu Val Ser Tyr
 -85 -80 -75

Gly Ile Asp Gly Leu Asp Glu Ile Val Gln Glu Leu Asn Ala Ala Asp
 -70 -65 -60 -55

Ala Val Pro Gly Val Val Gly Trp Tyr Pro Asp Val Ala Gly Asp Thr
 -50 -45 -40

Val Val Leu Glu Val Leu Glu Gly Ser Gly Ala Asp Val Ser Gly Leu
 -35 -30 -25

Leu Ala Asp Ala Gly Val Asp Ala Ser Ala Val Glu Val Thr Thr Ser
 -20 -15 -10

Asp Gln Pro Glu Leu Tyr Ala Asp Ile Ile Gly Gly Leu Ala Tyr Tyr
 -5 -1 1 5 10

Met Gly Gly Arg Cys Ser Val Gly Phe Ala Ala Thr Asn Ala Ser Gly
 15 20 25

Gln Pro Gly Phe Val Thr Ala Gly His Cys Gly Thr Val Gly Thr Pro
 30 35 40

Val Ser Ile Gly Asn Gly Lys Gly Val Phe Glu Arg Ser Ile Phe Pro
 45 50 55

Gly Asn Asp Ser Ala Phe Val Arg Gly Thr Ser Asn Phe Thr Leu Thr
 60 65 70

Asn Leu Val Ser Arg Tyr Asn Ser Gly Gly Tyr Ala Thr Val Ala Gly
 75 80 85 90

His Asn Gln Ala Pro Ile Gly Ser Ala Val Cys Arg Ser Gly Ser Thr
 95 100 105

Thr Gly Trp His Cys Gly Thr Ile Gln Ala Arg Asn Gln Thr Val Arg
 110 115 120

Tyr Pro Gln Gly Thr Val Tyr Ser Leu Thr Arg Thr Thr Val Cys Ala
 125 130 135

Glu Pro Gly Asp Ser Gly Gly Ser Tyr Ile Ser Gly Thr Gln Ala Gln
 140 145 150

Gly Val Thr Ser Gly Gly Ser Gly Asn Cys Ser Ala Gly Gly Thr Thr
 155 160 165 170

Tyr Tyr Gln Glu Val Asn Pro Met Leu Ser Ser Trp Gly Leu Thr Leu
 175 180 185

Arg Thr Gln Ser His Val Gln Ser Ala Pro
 190 195

<210> 46
 <211> 165
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Shuffled pro-peptide O-2.19

<220>
 <221> PROPEP
 <222> (1)..(165)

<400> 46

Ala Thr Gly Ala Leu Pro Gln Ser Pro Thr Pro Glu Ala Asp Ala Val
 1 5 10 15

Ser Met Gln Glu Ala Leu Gln Arg Asp Leu Asp Leu Thr Ser Ala Glu
 20 25 30

Ala Glu Glu Leu Leu Ala Ala Gln Asp Thr Ala Phe Glu Val Asp Glu
 35 40 45

Ala Ala Ala Ala Ala Ala Gly Asp Ala Tyr Gly Gly Ser Val Phe Asp
 50 55 60

Thr Glu Ser Leu Thr Leu Thr Val Leu Val Thr Asp Ala Ser Ala Val
 65 70 75 80

Glu Ala Val Glu Ala Ala Gly Ala Glu Ala Lys Val Val Ser His Gly

	85		90		95										
Met	Glu	Gly	Leu	Glu	Glu	Ile	Val	Ala	Asp	Leu	Asn	Ala	Ala	Asp	Ala
			100					105					110		
Gln	Pro	Gly	Val	Val	Gly	Trp	Tyr	Pro	Asp	Ile	His	Ser	Asp	Thr	Val
			115				120					125			
Val	Leu	Glu	Val	Leu	Glu	Gly	Ser	Gly	Ala	Asp	Val	Asp	Ser	Leu	Leu
	130					135					140				
Ala	Asp	Ala	Gly	Val	Asp	Ala	Ser	Ala	Val	Glu	Val	Thr	Thr	Ser	Asp
145					150					155					160
Gln	Pro	Glu	Leu	Tyr											
				165											
<210>	47														
<211>	166														
<212>	PRT														
<213>	Artificial sequence														
<220>															
<223>	Shuffled propeptide G-2.73														
<220>															
<221>	PROPEP														
<222>	(1)..(166)														
<400>	47														
Ala	Thr	Gly	Ala	Leu	Pro	Gln	Ser	Pro	Thr	Pro	Glu	Ala	Asp	Ala	Val
1				5					10					15	
Ser	Met	Gln	Glu	Ala	Leu	Gln	Arg	Asp	Leu	Asp	Leu	Ser	Ser	Ala	Glu
			20					25					30		
Ala	Glu	Glu	Leu	Leu	Ala	Ala	Gln	Asp	Thr	Ala	Phe	Glu	Val	Asp	Glu
			35				40					45			
Ala	Ala	Ala	Gly	Ala	Ala	Gly	Asp	Ala	Tyr	Gly	Gly	Ser	Val	Phe	Asp
	50					55					60				
Thr	Glu	Thr	Leu	Glu	Leu	Thr	Val	Leu	Val	Thr	Asp	Ala	Ser	Ala	Val
65					70					75					80

Glu Ala Val Glu Ala Ala Gly Ala Glu Ala Lys Val Val Ser His Gly
85 90 95

Met Glu Gly Leu Glu Glu Ile Val Ala Asp Leu Asn Ala Ala Asp Ala
100 105 110

Gln Pro Gly Val Val Gly Trp Tyr Pro Asp Ile His Ser Asp Thr Val
115 120 125

Val Val Glu Val Leu Glu Gly Ser Gly Ala Asp Val Asp Ser Leu Leu
130 135 140

Ala Asp Ala Gly Val Asp Thr Ala Asp Val Lys Val Glu Ser Thr Thr
145 150 155 160

Glu Gln Pro Glu Leu Tyr
165

<210> 48
<211> 166
<212> PRT
<213> Artificial sequence

<220>
<223> Shuffled propeptide G-1.43

<220>
<221> PROPEP
<222> (1)..(166)

<400> 48

Ala Thr Gly Ala Leu Pro Gln Ser Pro Thr Pro Glu Ala Asp Ala Val
1 5 10 15

Ser Met Gln Glu Ala Leu Gln Arg Asp Leu Gly Leu Ser Ser Ser Gln
20 25 30

Ala Glu Glu Leu Leu Asp Ala Gln Ala Glu Ser Phe Glu Ile Asp Glu
35 40 45

Ala Ala Ala Ala Ala Ala Gly Asp Ala Tyr Gly Gly Ser Ile Phe Asp
50 55 60

Thr Asp Ser Leu Thr Leu Thr Val Leu Val Thr Asp Ala Ser Ala Val

65 70 75 80
 Glu Ala Val Glu Ala Ala Gly Ala Glu Ala Lys Val Val Ser His Gly
 85 90 95
 Met Glu Gly Leu Glu Glu Ile Val Ala Asp Leu Asn Ala Ala Asp Ala
 100 105 110
 Gln Pro Gly Val Val Gly Trp Tyr Pro Asp Ile His Ser Asp Thr Val
 115 120 125
 Val Leu Glu Val Leu Glu Gly Ser Gly Ala Asp Val Asp Ser Leu Leu
 130 135 140
 Ala Asp Ala Gly Val Asp Thr Ala Asp Val Lys Val Glu Ser Thr Thr
 145 150 155 160
 Glu Gln Pro Glu Leu Tyr
 165

<210> 49
 <211> 166
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Shuffled propeptide G-2.6

<220>
 <221> PROPEP
 <222> (1)..(166)

<400> 49

Ala Thr Gly Ala Leu Pro Gln Ser Pro Thr Pro Glu Ala Asp Ala Val
 1 5 10 15
 Ser Met Gln Glu Ala Leu Gln Arg Asp Leu Asp Leu Thr Ser Ala Glu
 20 25 30
 Ala Glu Glu Leu Leu Ala Ala Gln Asp Thr Ala Phe Glu Val Asp Glu
 35 40 45
 Ala Ala Ala Ala Ala Ala Gly Asp Ala Tyr Gly Gly Ser Ile Phe Asp
 50 55 60

Thr Glu Thr Leu Glu Leu Thr Val Leu Val Thr Asp Ser Ser Ser Val
65 70 75 80

Glu Ala Val Glu Ala Ala Gly Ala Glu Ala Lys Val Val Ser His Gly
85 90 95

Met Glu Gly Leu Glu Glu Ile Val Ala Asp Leu Asn Ala Ala Asp Ala
100 105 110

Gln Pro Gly Val Val Gly Trp Tyr Pro Asp Ile His Ser Asp Thr Val
115 120 125

Val Leu Glu Val Leu Glu Gly Ser Gly Ala Asp Val Asp Ser Leu Leu
130 135 140

Ala Gly Ala Gly Val Asp Thr Ala Asp Val Lys Val Glu Ser Thr Thr
145 150 155 160

Glu Gln Pro Glu Leu Tyr
165

<210> 50
<211> 165
<212> PRT
<213> Artificial sequence

<220>
<223> Shuffled propeptide G-2.5

<220>
<221> PROPEP
<222> (1)..(165)

<400> 50

Ala Thr Gly Ala Leu Pro Gln Ser Pro Thr Pro Glu Ala Asp Ala Val
1 5 10 15

Ser Met Gln Glu Ala Leu Gln Arg Asp Leu Gly Leu Thr Pro Leu Glu
20 25 30

Ala Glu Glu Leu Leu Ala Ala Gln Asp Thr Ala Phe Glu Val Asp Glu
35 40 45

Ala Ala Ala Glu Ala Ala Gly Asp Ala Tyr Gly Gly Ser Val Phe Asp

Glu Ala Ala Ala Ala Ala Ala Gly Asp Ala Tyr Gly Gly Ser Ile Phe
 50 55 60

Asp Thr Asp Ser Leu Thr Leu Thr Val Leu Val Thr Asp Ala Ala Ala
 65 70 75 80

Val Glu Ala Val Glu Ala Ala Gly Ala Glu Ala Lys Val Val Ser His
 85 90 95

Gly Met Glu Gly Leu Glu Glu Ile Val Ala Asp Leu Asn Ala Ala Asp
 100 105 110

Ala Val Pro Gly Val Val Gly Trp Tyr Pro Asp Val Ala Gly Asp Thr
 115 120 125

Val Val Leu Glu Val Leu Glu Gly Ser Gly Ala Asp Val Tyr Ser Leu
 130 135 140

Leu Ala Asp Ala Gly Val Asp Ala Ser Ala Val Glu Val Thr Pro Ala
 145 150 155 160

Ala Gln Pro Glu Leu Tyr
 165

<210> 52
 <211> 166
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Shuffled propeptide G-1.4

<220>
 <221> PROPEP
 <222> (1)..(166)

<400> 52

Ala Thr Gly Ala Leu Pro Gln Ser Pro Thr Pro Glu Ala Asp Ala Val
 1 5 10 15

Ser Met Gln Glu Ala Leu Gln Arg Asp Leu Gly Leu Ser Ser Ser Gln
 20 25 30

Ala Glu Glu Leu Leu Asp Ala Gln Ala Glu Ser Phe Glu Ile Asp Glu

35	40	45
Ala Ala Ala Ala Ala Ala Ala Asp Ser Tyr Gly Gly Ser Ile Phe Asp		
50	55	60
Thr Asp Ser Leu Thr Leu Thr Val Leu Val Thr Asp Ala Ser Ala Val		
65	70	75 80
Glu Ala Val Glu Ala Ala Gly Ala Glu Ala Lys Val Val Ser His Gly		
85	90	95
Met Glu Gly Leu Glu Glu Ile Val Ala Asp Leu Asn Ala Ala Asp Ala		
100	105	110
Gln Pro Gly Val Val Gly Trp Tyr Pro Asp Ile His Ser Asp Thr Val		
115	120	125
Val Leu Glu Val Leu Glu Gly Ser Gly Ala Asp Val Asp Ser Leu Leu		
130	135	140
Ala Asp Ala Gly Val Asp Thr Ala Asp Val Lys Val Glu Ser Thr Thr		
145	150	155 160
Glu Gln Pro Glu Leu Tyr		
165		

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<220>
 <223> Shuffled propeptide G-1.2

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<400> 53

Ala Thr Gly Ala Leu Pro Gln Ser Pro Thr Pro Glu Ala Asp Ala Val
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Ser Met Gln Glu Ala Leu Gln Arg Asp Leu Asp Leu Thr Ser Ala Glu
20 25 30

Ala Glu Glu Leu Leu Ala Ala Gln Asp Thr Ala Phe Glu Val Asp Glu
 35 40 45

Ala Ala Ala Ala Ala Ala Gly Asp Ala Tyr Gly Gly Ser Ile Phe Asp
 50 55 60

Thr Glu Thr Leu Glu Leu Thr Val Leu Val Thr Asp Ser Ser Ser Val
 65 70 75 80

Glu Ala Val Glu Ala Ala Gly Ala Glu Ala Lys Val Val Ser His Gly
 85 90 95

Met Glu Gly Leu Glu Glu Ile Val Ala Asp Leu Asn Ala Ala Asp Ala
 100 105 110

Gln Pro Gly Val Val Gly Trp Tyr Pro Asp Ile His Ser Asp Thr Val
 115 120 125

Val Leu Glu Val Leu Glu Gly Ser Gly Ala Asp Val Asp Ser Leu Leu
 130 135 140

Ala Gly Ala Gly Val Asp Thr Ala Asp Val Lys Val Glu Ser Thr Thr
 145 150 155 160

Glu Gln Pro Glu Leu Tyr
 165